

## (1) GENERAL INFORMATION

- (2) INFORMATION FOR SEQ ID NO:1:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr  
1 5 10 15  
Arg Pro Ala Pro  
20

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCTCCACCG CCCCCCAGC CCACGGTGTC ACCTCGGCCC CGGACACCAG GCCGGCCCCG 60

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Pro Asp Thr Arg Pro Ala Pro  
1 5

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGCAGTACTG CACCACCGGC ACATGGCGTA ACATCAGCAC CTGATACAAG ACCTGCACCT 60

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGATCCACCG CGCCGCCTGC GCACGGAGTG ACGTCGGCGC CCGACACGCG CCCCCTCCC 60

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGTCAACAG CTCCTCCCGC TCATGGGGTT ACTTCTGCTC CAGATACTCG CCCAGCTCCA 60

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTTCGACGG CCCCCCTGC TCACGGTGTA ACATCCGCCC CGGATACCAG ACCGGCCCCCT 60

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCAGCACCG CACCGCCCGC ACACGGGGTC ACAAGCGCGC CAGACACTCG ACCTGCGCCA 60

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGAAGTACCG CTCCACCTGC ACACGGGGTC ACAAGCGCGC CAGACACTCG ACCTGCGCCA 60

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGTCGACTG CCCCTCCGGC GCATGGTGTG ACCTCAGCTC CTGACACAAG GCCAGCCCCA 60

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## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGTCAACGG CACCTCCAGC ACACGGAGTC ACGTCTGCAC CCGACACCCG TCCAGCTCCG 60

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTAGTACAG CGCCACCCGC ACATGGCGTC ACGAGCGCTC CGGATACGAG ACCGGCGCCT 60

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGCTCCACCG CACCCCCAGC CCACGGTGTC ACCTCGGCCC CGGACACCAG GCGGGCCCCG 60  
GGCTCCACCG CGGCCCCG 78

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCTCCACCG CCCCCCAGC CCATGGTGTC ACCTCGGCCC CGGACAACAG GCCCGCCTTG 60

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGCTCCACCG CCCCTCCAGT CCACAATGTC ACCTCGGCC

39

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr
1				5				10						15	
Arg	Arg	Ala	Pro												
				20											

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Asn
1				5				10						15	
Arg	Pro	Ala	Leu												
				20											

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly	Ser	Thr	Ala	Pro	Pro	Val	His	Asn	Val	Thr	Ser	Ala
1				5				10				

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...1524  
 (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG ACA CCG GGC ACC CAG TCT CCT TTC TTC CTG CTG CTG CTC CTC ACA	48
Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Thr	
1 5 10 15	
GTG CTT ACA GCT ACC ACA GCC CCT AAA CCC GCA ACA GTT GTT ACG GGT	96
Val Leu Thr Ala Thr Thr Ala Pro Lys Pro Ala Thr Val Val Thr Gly	
20 25 30	
TCT GGT CAT GCA AGC TCT ACC CCA GGT GGA GAA AAG GAG ACT TCG GCT	144
Ser Gly His Ala Ser Ser Thr Pro Gly Gly Glu Lys Glu Thr Ser Ala	
35 40 45	
ACC CAG AGA AGT TCA GTG CCC AGC TCT ACT GAG AAG AAT GCT GTG AGT	192
Thr Gln Arg Ser Ser Val Pro Ser Ser Thr Glu Lys Asn Ala Val Ser	
50 55 60	
ATG ACA AGC TTG ATA TCG AAT TCC GGT GTC CGG GGC TCC ACC GCC CCC	240
Met Thr Ser Leu Ile Ser Asn Ser Gly Val Arg Gly Ser Thr Ala Pro	
65 70 75 80	
CCA GCC CAC GGT GTC ACC TCG GCC CCG GAC ACC AGG CCG GCC CCG GGC	288
Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly	
85 90 95	
TCC ACC GCC CCC CCA GCC CAC GGT GTC ACC TCG GCC CCG GAC ACC AGG	336
Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg	
100 105 110	
CCG GCC CCG GGC TCC ACC GCC CCC CCA GCC CAC GGT GTC ACC TCG GCC	384
Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala	
115 120 125	
CCG GAC ACC AGG CCG GCC CCG GGC TCC ACC GCA CCC CCA GCC CAC GGT	432
Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly	
130 135 140	
GTC ACC TCG GCC CCG GAC ACC AGG CGG GCC CCG GGC TCC ACC CCG GCC	480
Val Thr Ser Ala Pro Asp Thr Arg Arg Ala Pro Gly Ser Thr Pro Ala	
145 150 155 160	
CCG GGC TCC ACC GCC CCC CCA GCC CAC GGT GTC ACC TCG GCC CCG GAC	528
Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp	
165 170 175	
ACC AGG CCG GCC CCG GGC TCC ACC GCC CCC CCA GCC CAT GGT GTC ACC	576
Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr	
180 185 190	
TCG GCC CCG GAC AAC AGG CCC GCC TTG GGC TCC ACC GCC CCT CCA GTC	624
Ser Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser Thr Ala Pro Pro Val	
195 200 205	

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CAC AAT GTC ACC TCG GCC TCA GGC TCT GCA TCA GGC TCA GCT TCT ACT	672
His Asn Val Thr Ser Ala Ser Gly Ser Ala Ser Gly Ser Ala Ser Thr	
210 215 220	
CTG GTG CAC AAC GGC ACC TCT GCC AGG GCT ACC ACA ACC CCA GCC AGC	720
Leu Val His Asn Gly Thr Ser Ala Arg Ala Thr Thr Thr Pro Ala Ser	
225 230 235 240	
AAG AGC ACT CCA TTC TCA ATT CCC AGC CAC CAC TCT GAT ACT CCT ACC	768
Lys Ser Thr Pro Phe Ser Ile Pro Ser His His Ser Asp Thr Pro Thr	
245 250 255	
ACC CTT GCC AGC CAT AGC ACC AAG ACT GAT GCC AGT AGC ACT CAC CAT	816
Thr Leu Ala Ser His Ser Thr Lys Thr Asp Ala Ser Ser Thr His His	
260 265 270	
AGC ACG GTA CCT CCT CTC ACC TCC TCC AAT CAC AGC ACT TCT CCC CAG	864
Ser Thr Val Pro Pro Leu Thr Ser Ser Asn His Ser Thr Ser Pro Gln	
275 280 285	
TTG TCT ACT GGG GTC TCT TTC TTT TTC CTG TCT TTT CAC ATT TCA AAC	912
Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn	
290 295 300	
CTC CAG TTT CCT TCC TCT CTC GAA GAT CCC AGC ACC GAC TAC TAC CAA	960
Leu Gln Phe Pro Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln	
305 310 315 320	
GAG CTG CAG AGA GAC ATT TCT CAA ATG TTT TTG CAG ATT TAT AAA CAA	1008
Glu Leu Gln Arg Asp Ile Ser Gln Met Phe Leu Gln Ile Tyr Lys Gln	
325 330 335	
GGG GGT TTT CTG GGC CTC TCC AAT ATT AAG TTC AGG CCA GGA TCT GTG	1056
Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val	
340 345 350	
CTG GTA CAA TTG ACT CTG GCC TTC CGA GAA GGT ACC ATC AAT GTC CAC	1104
Leu Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His	
355 360 365	
GAC GTG GAG ACA CAG TTC AAT CAG TAT AAA ACG GAA GCA GCC TCT CGA	1152
Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg	
370 375 380	
TAT AAC CTG ACG ATC CCA GAC GTC AGC GTG AGT GAT GTG CCA TTT CCT	1200
Tyr Asn Leu Thr Ile Pro Asp Val Ser Val Ser Asp Val Pro Phe Pro	
385 390 395 400	
TTC TCT GCC CAG TCT GGG GCT GGG GTG CCA GGC TGG GGC ATC GCG CTG	1248
Phe Ser Ala Gln Ser Gly Ala Gly Val Pro Gly Trp Gly Ile Ala Leu	
405 410 415	
CTC CTG CTG GTC TGT GTT CTG GTT GCG CTG GCC ATT GTC TAT CTC ATT	1296
Leu Leu Leu Val Cys Val Leu Val Ala Leu Ala Ile Val Tyr Leu Ile	
420 425 430	
GCC TTG GCT GTC TGT CAG TGC CGC CGA AAG AAC TAC GGG CAG CTG GAC	1344
Ala Leu Ala Val Cys Gln Cys Arg Arg Lys Asn Tyr Gly Gln Leu Asp	
435 440 445	

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ATC TTT CCA GCC CGG GAT ACC TAC CAT CCT ATG AGC GAG TAC CCC ACC 1392  
 Ile Phe Pro Ala Arg Asp Thr Tyr His Pro Met Ser Glu Tyr Pro Thr  
 450 455 460

TAC CAC ACC CAT GGG CGC TAT GTC CCC CCT AGC AGT ACC GAT CGT AGC 1440  
 Tyr His Thr His Gly Arg Tyr Val Pro Pro Ser Ser Thr Asp Arg Ser  
 465 470 475 480

CCC TAT GAG AAG GTT TCT GCA GGT AAT GGT GGC AGC AGC CTC TCT TAC 1488  
 Pro Tyr Glu Lys Val Ser Ala Gly Asn Gly Gly Ser Ser Leu Ser Tyr  
 485 490 495

ACA AAC CCA GCA GTG GCA GCC ACT TCT GCC AAC TTG TAG 1527  
 Thr Asn Pro Ala Val Ala Ala Thr Ser Ala Asn Leu  
 500 505

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr  
 1 5 10 15  
 Val Leu Thr Ala Thr Thr Ala Pro Lys Pro Ala Thr Val Val Thr Gly  
 20 25 30  
 Ser Gly His Ala Ser Ser Thr Pro Gly Gly Glu Lys Glu Thr Ser Ala  
 35 40 45  
 Thr Gln Arg Ser Ser Val Pro Ser Ser Thr Glu Lys Asn Ala Val Ser  
 50 55 60  
 Met Thr Ser Leu Ile Ser Asn Ser Gly Val Arg Gly Ser Thr Ala Pro  
 65 70 75 80  
 Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly  
 85 90 95  
 Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg  
 100 105 110  
 Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala  
 115 120 125  
 Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly  
 130 135 140  
 Val Thr Ser Ala Pro Asp Thr Arg Arg Ala Pro Gly Ser Thr Pro Ala  
 145 150 155 160  
 Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp  
 165 170 175  
 Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr  
 180 185 190  
 Ser Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser Thr Ala Pro Pro Val  
 195 200 205  
 His Asn Val Thr Ser Ala Ser Gly Ser Ala Ser Gly Ser Ala Ser Thr  
 210 215 220  
 Leu Val His Asn Gly Thr Ser Ala Arg Ala Thr Thr Thr Pro Ala Ser  
 225 230 235 240  
 Lys Ser Thr Pro Phe Ser Ile Pro Ser His His Ser Asp Thr Pro Thr

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Thr	Leu	Ala	Ser	His	Ser	Thr	Lys	Thr	Asp	Ala	Ser	Ser	Thr	His	His
Ser	Thr	Val	Pro	Pro	Leu	Thr	Ser	Ser	Asn	His	Ser	Thr	Ser	Pro	Gln
Leu	Ser	Thr	Gly	Val	Ser	Phe	Phe	Phe	Leu	Ser	Phe	His	Ile	Ser	Asn
Leu	Gln	Phe	Pro	Ser	Ser	Leu	Glu	Asp	Pro	Ser	Thr	Asp	Tyr	Tyr	Gln
Glu	Leu	Gln	Arg	Asp	Ile	Ser	Gln	Met	Phe	Leu	Gln	Ile	Tyr	Lys	Gln
Gly	Gly	Phe	Leu	Gly	Leu	Ser	Asn	Ile	Lys	Phe	Arg	Pro	Gly	Ser	Val
Leu	Val	Gln	Leu	Thr	Leu	Ala	Phe	Arg	Glu	Gly	Thr	Ile	Asn	Val	His
Asp	Val	Glu	Thr	Gln	Phe	Asn	Gln	Tyr	Lys	Thr	Glu	Ala	Ala	Ser	Arg
Tyr	Asn	Leu	Thr	Ile	Pro	Asp	Val	Ser	Val	Ser	Asp	Val	Pro	Phe	Pro
Phe	Ser	Ala	Gln	Ser	Gly	Ala	Gly	Val	Pro	Gly	Trp	Gly	Ile	Ala	Leu
Leu	Leu	Leu	Val	Cys	Val	Leu	Val	Ala	Leu	Ala	Ile	Val	Tyr	Leu	Ile
Ala	Leu	Ala	Val	Cys	Gln	Cys	Arg	Arg	Lys	Asn	Tyr	Gly	Gln	Leu	Asp
Ile	Phe	Pro	Ala	Arg	Asp	Thr	Tyr	His	Pro	Met	Ser	Glu	Tyr	Pro	Thr
Tyr	His	Thr	His	Gly	Arg	Tyr	Val	Pro	Pro	Ser	Ser	Thr	Asp	Arg	Ser
Pro	Tyr	Glu	Lys	Val	Ser	Ala	Gly	Asn	Gly	Gly	Ser	Ser	Leu	Ser	Tyr
Thr	Asn	Pro	Ala	Val	Ala	Ala	Thr	Ser	Ala	Asn	Leu				